Appl. No. 09/597,796
Amdt. dated December 22, 2004
Reply to Office Action of August 25, 2004

PATENT

Amendments to the Specification:

Please amend the paragraph on page 1, line 5, as follows:

-- The present application is a continuation-in-part of U.S. patent application No. 09/287,849, filed April 7, 1999, now U.S. Patent No. 6,627,198, which is a continuation-in-part of U.S. patent application No. 09/223,040, filed December 30, 1998, now U.S. Patent No. 6,580,058, which is continuation-in-part of U.S. patent application No. 09/056,556, filed April 7, 1998, now U.S. Patent No. 6,350,456, which claims priority to ~~U.S. patent application No. 09/056,556, filed April 7, 1998; U.S. patent application No. 09/223,040, filed December 30, 1998; U.S. patent application No. 09/287,849, filed April 7, 1999; and published PCT application No. WO99/51748, filed April 7, 1999 (PCT/US99/07717)~~, U.S. patent application No. 60/158,338, filed October 7, 1999, and U.S. application No. 60/158,425, filed October 7, 1999 herein each incorporated by reference in its entirety.--

Please amend the paragraph beginning on page 8, line 5, as follows:

--Each of the above sequences is also disclosed in Cole *et al. Nature* 393:537 (1998) ~~and can be found at, e.g., http://www.sanger.ac.uk and http:/www.pasteur.fr/mycdb/~~.--

Please amend the paragraph beginning on page 8, line 25, as follows:

--"Fusion polypeptide" or "fusion protein" refers to a protein having at least two heterologous *Mycobacterium* sp. polypeptides covalently linked, either directly or via an amino acid linker. The polypeptides forming the fusion protein are typically linked C-terminus to N-terminus, although they can also be linked C-terminus to C-terminus, N-terminus to N-terminus, or N-terminus to C-terminus. The polypeptides of the fusion protein can be in any order. This term also refers to conservatively modified variants, polymorphic variants, alleles, mutants, subsequences, and interspecies homologs of the antigens that make up the fusion protein. *Mycobacterium tuberculosis* antigens are described in Cole *et al., Nature* 393:537 (1998), which discloses the entire *Mycobacterium tuberculosis* genome. ~~The complete sequence of~~

Appl. No. 09/597,796
Amdt. dated December 22, 2004
Reply to Office Action of August 25, 2004

PATENT

~~*Mycobacterium tuberculosis*~~ ~~can also be found at http://www.sanger.ac.uk and at~~

~~http://www.pasteur.fr/mycdb/ (MycDB).~~ Antigens from other *Mycobacterium* species that

correspond to *M. tuberculosis* antigens can be identified, e.g., using sequence comparison

algorithms, as described herein, or other methods known to those of skill in the art, e.g.,

hybridization assays and antibody binding assays.--

Please amend the paragraph beginning on page 17, line 28, as follows:

-- Another example of algorithm that is suitable for determining percent sequence

identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described

in Altschul *et al., Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul *et al., J. Mol. Biol.*

215:403-410 (1990), respectively. Software for performing BLAST analyses is publicly

available through the National Center for Biotechnology Information

~~(http://www.ncbi.nlm.nih.gov/)~~. This algorithm involves first identifying high scoring sequence

pairs (HSPs) by identifying short words of length W in the query sequence, which either match

or satisfy some positive-valued threshold score T when aligned with a word of the same length in

a database sequence. T is referred to as the neighborhood word score threshold (Altschul *et al.,*

supra). These initial neighborhood word hits act as seeds for initiating searches to find longer

HSPs containing them. The word hits are extended in both directions along each sequence for as

far as the cumulative alignment score can be increased. Cumulative scores are calculated using,

for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always

> 0) and N (penalty score for mismatching residues; always < 0). For amino acid sequences, a

scoring matrix is used to calculate the cumulative score. Extension of the word hits in each

direction are halted when: the cumulative alignment score falls off by the quantity X from its

maximum achieved value; the cumulative score goes to zero or below, due to the accumulation

of one or more negative-scoring residue alignments; or the end of either sequence is reached.

The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the

alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W)

of 11, an expectation (E) or 10, M=5, N=-4 and a comparison of both strands. For amino acid

sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10,

Appl. No. 09/597,796
Amdt. dated December 22, 2004
Reply to Office Action of August 25, 2004

PATENT

and the BLOSUM62 scoring matrix (*see* Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=-4, and a comparison of both strands.--